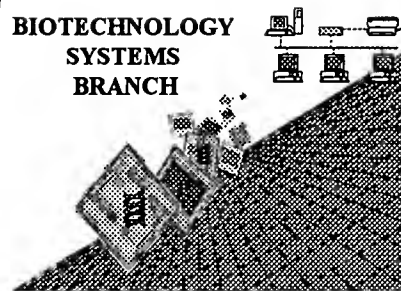


Wessendy

#4

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/096,749

Art Unit / Team No. :

1642

Date Processed by STIC:

9/9/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

#4/AL
10/19/98

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/096,749

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
- 7 ☒ Wrong Designation Sequence(s) 110 contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of N's or Xaa's (NEW RULES) Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 ☐ Wrong Format File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures" Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620 applies to applications filed on or after July 1, 1998.
AKS-Biotechnology Systems Branch- 7/10/98

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/096,749DATE: 09/09/98
TIME: 15:58:54

INPUT SET: S28504.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Koieda, Shohei
6
7 (ii) TITLE OF THE INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
8
9 (iii) NUMBER OF SEQUENCES: 118
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
13 (B) STREET: 121 South Eighth Street, Ste. 1600
14 (C) CITY: Minneapolis
15 (D) STATE: MN
16 (E) COUNTRY: USA
17 (F) ZIP: 55402
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Diskette
21 (B) COMPUTER: IBM Compatible
22 (C) OPERATING SYSTEM: DOS
23 (D) SOFTWARE: FastSEQ Version 2.0b
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: 09/096,749
27 (B) FILING DATE: June 12, 1998
28
29 (vii) PRIOR APPLICATION DATA:
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Ann S. Viksnins
35 (B) REGISTRATION NUMBER: 37,748
36 (C) REFERENCE/DOCKET NUMBER: 109.034US1
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: (612) 373-6900
40 (B) TELEFAX: (612) 339-3061
41
42

ERRORED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/096,749DATE: 09/09/98
TIME: 15:58:55

INPUT SET: S28504.raw

273 (2) INFORMATION FOR SEQ ID NO:13:
274
275 (i) SEQUENCE CHARACTERISTICS:
--> 276 (A) LENGTH: 59 base pairs
277 (B) TYPE: nucleic acid
278 (C) STRANDEDNESS: single
279 (D) TOPOLOGY: linear
280
281 (ii) MOLECULE TYPE: cDNA
282 (iii) HYPOTHETICAL: NO
283 (iv) ANTI-SENSE: NO
284 (v) FRAGMENT TYPE:
285 (vi) ORIGINAL SOURCE:
286
287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
288
289 CGGGATCCCA TATGCAGGTT TCTGATGTTT CGCGTGACCT GGAAGTTGTT
--> 290 GCTGCGACC 59
291

*format error - see
line 1 on Eva summary
sheet*

59

292 (2) INFORMATION FOR SEQ ID NO:14:
293
294 (i) SEQUENCE CHARACTERISTICS:
--> 295 (A) LENGTH: 55 base pairs
296 (B) TYPE: nucleic acid
297 (C) STRANDEDNESS: single
298 (D) TOPOLOGY: linear
299
300 (ii) MOLECULE TYPE: cDNA
301 (iii) HYPOTHETICAL: NO
302 (iv) ANTI-SENSE: NO
303 (v) FRAGMENT TYPE:
304 (vi) ORIGINAL SOURCE:
305
306 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
307
308 TAACTGCAGG AGCATCCAG CTGATCAGCA GGCTAGTCGG GGTGCGAGCA
--> 309 ACAAC 55
310

*same
error*

311 (2) INFORMATION FOR SEQ ID NO:15:
312
313 (i) SEQUENCE CHARACTERISTICS:
--> 314 (A) LENGTH: 51 base pairs
315 (B) TYPE: nucleic acid
316 (C) STRANDEDNESS: single
317 (D) TOPOLOGY: linear
318
319 (ii) MOLECULE TYPE: cDNA
320 (iii) HYPOTHETICAL: NO
321 (iv) ANTI-SENSE: NO
322 (v) FRAGMENT TYPE:
323 (vi) ORIGINAL SOURCE:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/096,749DATE: 09/09/98
TIME: 15:58:56

INPUT SET: S28504.raw

324
325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
326
327 CTCCTGCAGT TACCGTGCGT TATTACCGTA TCACGTACGG TGAAACCGGT G
328 51
329

Same

402 (2) INFORMATION FOR SEQ ID NO:20:
403

404 (i) SEQUENCE CHARACTERISTICS:
--> 405 (A) LENGTH: 55 base pairs
406 (B) TYPE: nucleic acid
407 (C) STRANDEDNESS: single
408 (D) TOPOLOGY: linear
409
410 (ii) MOLECULE TYPE: cDNA
411 (iii) HYPOTHETICAL: NO
412 (iv) ANTI-SENSE: NO
413 (v) FRAGMENT TYPE:
414 (vi) ORIGINAL SOURCE:
415
416 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
417
418 CGGGATCCGA GCTCGCTGGG CTGTCACCAC GGCCAGTAAC AGCGTATACA
--> 419 GTGAT 55
420

Same

529 (2) INFORMATION FOR SEQ ID NO:27:
530

531 (i) SEQUENCE CHARACTERISTICS:
--> 532 (A) LENGTH: 51 base pairs
533 (B) TYPE: nucleic acid
534 (C) STRANDEDNESS: single
535 (D) TOPOLOGY: linear
536
537 (ii) MOLECULE TYPE: cDNA
538 (iii) HYPOTHETICAL: NO
539 (iv) ANTI-SENSE: NO
540 (v) FRAGMENT TYPE:
541 (vi) ORIGINAL SOURCE:
542
543 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
544
545 GATCAGCTGG GATGCTCCTN NKNNKNNKNN KNNKTATTAC CGTATCACGT A
546 51
547

Same

548 (2) INFORMATION FOR SEQ ID NO:28:
549

550 (i) SEQUENCE CHARACTERISTICS:
--> 551 (A) LENGTH: 57 base pairs
552 (B) TYPE: nucleic acid
553 (C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/096,749DATE: 09/09/98
TIME: 15:58:57

INPUT SET: S28504.raw

554 (D) TOPOLOGY: linear
555
556 (ii) MOLECULE TYPE: cDNA
557 (iii) HYPOTHETICAL: NO
558 (iv) ANTI-SENSE: NO
559 (v) FRAGMENT TYPE:
560 (vi) ORIGINAL SOURCE:
561
562 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
563
564 TGTATACGCT GTTACTGGCN NKNNKNNKNN KNNKNNKNNK TCCAAGCCAA
--> 565 TCTCGAT 57
566

same

567 (2) INFORMATION FOR SEQ ID NO:29:
568
569 (i) SEQUENCE CHARACTERISTICS:
--> 570 (A) LENGTH: 47 base pairs
571 (B) TYPE: nucleic acid
572 (C) STRANDEDNESS: single
573 (D) TOPOLOGY: linear
574
575 (ii) MOLECULE TYPE: cDNA
576 (iii) HYPOTHETICAL: NO
577 (iv) ANTI-SENSE: NO
578 (v) FRAGMENT TYPE:
579 (vi) ORIGINAL SOURCE:
580
581 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
582
583 CTGTATACGC TGTTACTGGC NNKNNKNNKN NKCCAGCGAG CTCCAAG
584 47
585

same

586 (2) INFORMATION FOR SEQ ID NO:30:
587
588 (i) SEQUENCE CHARACTERISTICS:
--> 589 (A) LENGTH: 51 base pairs
590 (B) TYPE: nucleic acid
591 (C) STRANDEDNESS: single
592 (D) TOPOLOGY: linear
593
594 (ii) MOLECULE TYPE: cDNA
595 (iii) HYPOTHETICAL: NO
596 (iv) ANTI-SENSE: NO
597 (v) FRAGMENT TYPE:
598 (vi) ORIGINAL SOURCE:
599
600 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
601
602 CATCACTGTA TACGCTGTTA CTNNKNNKNN KNNKNNKTCC AAGCCAATCT C
603 51
604

same

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/096,749DATE: 09/09/98
TIME: 15:58:57

INPUT SET: S28504.raw

2099 (2) INFORMATION FOR SEQ ID NO:110:
2100
2101 (i) SEQUENCE CHARACTERISTICS:
--> 2102 (A) LENGTH: 94 amino acids
2103 (B) TYPE: amino acid
2104 (C) STRANDEDNESS: single
2105 (D) TOPOLOGY: linear
2106
2107 (ii) MOLECULE TYPE: peptide
2108 (iii) HYPOTHETICAL: NO
2109 (iv) ANTI-SENSE: NO
2110 (v) FRAGMENT TYPE: internal
2111 (vi) ORIGINAL SOURCE:
2112
2113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
2114
2115
2116 Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu
2117 1 5 10 15
2118 Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu
2119 20 25 30 35
--> 2120 Thr Gly Gly Asn Ser Pro Val Oxx Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala
2121 40 45 50 55
2122 Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr
2123 60 65 70 75
2124 Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr
2125 80 85 90
2126

involved amino acid - see 1.822(b) of

2127 (2) INFORMATION FOR SEQ ID NO:111:
2128
2129 (i) SEQUENCE CHARACTERISTICS:
--> 2130 (A) LENGTH: 248 base pairs
2131 (B) TYPE: nucleic acid
2132 (C) STRANDEDNESS: single
2133 (D) TOPOLOGY: linear
2134
2135 (ii) MOLECULE TYPE: cDNA
2136 (iii) HYPOTHETICAL: NO
2137 (iv) ANTI-SENSE: NO
2138 (v) FRAGMENT TYPE:
2139 (vi) ORIGINAL SOURCE:
2140
2141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:
2142
2143 CTGCTGATCA GCTGGGATGC TCCTGCAGTT ACCGTGCGTT ATTACCGTAT
2144 CACGTACGGT
2145
2146 GAAACCGGTG GTAAC TCCCC GGTT CAGGAA TTC ACTGTAC CTGGTTCCAA
2147 GTCTACTGCT
2148
2149 ACCATCAGCG GCCTGAAACC GGGTGTCGAC TATACCATCA CTGTATACGC

Sequence Rules
(see item
7 on Enon
summary
sheet)

60 where are
cumulative
base totals
at end of
each line?
— —

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/096,749DATE: 09/09/98
TIME: 15:58:58

INPUT SET: S28504.raw

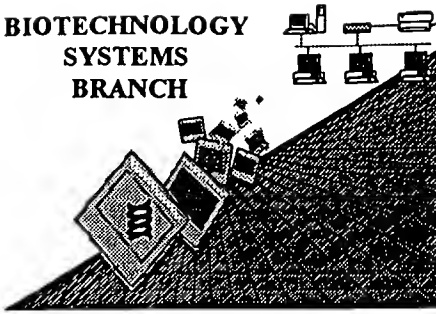
2150 TGTTACTGGC
2151
2152 CGTGGTGACA GCCCAGCGAG CTCCAAGCCA ATCTCGATTA ACTACCGTAC
2153 CTAGTAACTC
2154
--> 2155 GAGGATCC

248

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/096,749DATE: 09/09/98
TIME: 15:59:02**INPUT SET: S28504.raw**

Line	Error	Original Text
276	Entered (59) and Calc. Seq. Length (9) differ	(A) LENGTH: 59 base pairs
290	# of Sequences for line conflicts w/ running total	GCTGCGACC 59
295	Entered (55) and Calc. Seq. Length (5) differ	(A) LENGTH: 55 base pairs
309	# of Sequences for line conflicts w/ running total	ACAAC 55
314	Entered (51) and Calc. Seq. Length (0) differ	(A) LENGTH: 51 base pairs
405	Entered (55) and Calc. Seq. Length (5) differ	(A) LENGTH: 55 base pairs
419	# of Sequences for line conflicts w/ running total	GTGAT 55
532	Entered (51) and Calc. Seq. Length (0) differ	(A) LENGTH: 51 base pairs
551	Entered (57) and Calc. Seq. Length (7) differ	(A) LENGTH: 57 base pairs
565	# of Sequences for line conflicts w/ running total	TCTCGAT 57
570	Entered (47) and Calc. Seq. Length (0) differ	(A) LENGTH: 47 base pairs
589	Entered (51) and Calc. Seq. Length (0) differ	(A) LENGTH: 51 base pairs
2102	Entered (94) and Calc. Seq. Length (93) differ	(A) LENGTH: 94 amino acids
2120	Wrong Amino Acid Designator	Thr Gly Gly Asn Ser Pro Val Oxx Glu Phe Thr Val Pro Gly
2130	Entered (248) and Calc. Seq. Length (8) differ	(A) LENGTH: 248 base pairs
2155	# of Sequences for line conflicts w/ running total	GAGGATCC

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Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825).

Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: [pub/checker/](ftp://ftp.uspto.gov/pub/checker/)
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

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PTO Deposit Account

*For Further Information, Contact: **Arti Shah at 703-308-4212***